

## SEQUENCE LISTING

<110> LEE, Sang-Yup  
JEONG, Ki-Jun

<120> ESCHERICHIA COLI STRAIN SECRETING HUMAN  
GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)

<130> HYLEE60.001APC

<140> US 10/009,792

<141> 2001-11-13

<150> PCT/KR01/00549

<151> 2001-03-31

<150> KR 10-2000-0017052

<151> 2000-03-31

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<210> 1

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gaattcatat gactccgtta ggtccagcca gc

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ggctggacct aacggagttg cagaggcgg

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gcaaccgcct ctgcaactcc gttaggtcca gcc

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<400> 15  
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 agcttcctgc tcaagtgctt agagcaagtg aggaagatcc aggcgatgg cgcagcgctc 180  
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Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
50 55 60
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65 70 75 80
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
85 90 95
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
100 105 110
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
115 120 125
Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
130 135 140
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145 150 155 160
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170

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<210> 20  
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aagctgtgcc accccgagga gctgggtgctg ctccggacact ctccgggcat cccctgggct 180
cccctgagca gctgccccag ccaggccctg cagctggcag gctgcttgag ccaactccat 240
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cagatggaag aactgggaat ggccccctgcc ctgcagccca cccagggtgc catgccggcc 420
ttcgctctg ctttcagcg ccgggcagga ggggtcctag ttgctccca tctgcagagc 480
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<210> 21

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 20 25 30  
 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu  
 35 40 45  
 Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser  
 50 55 60  
 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His  
 65 70 75 80  
 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
 85 90 95  
 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala  
 100 105 110  
 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala  
 115 120 125  
 Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala  
 130 135 140  
 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser  
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 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 165 170 175

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<210> 23  
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<400> 23  
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<400> 24  
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 ttctgtctca agtgc 135

<210> 25  
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 <212> PRT  
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<400> 25  
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 Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Thr Pro Leu Gly  
 20 25 30  
 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys  
 35 40 45

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 aggactccgt taggtccagc cagctccctg cccagagct tcc:gctcaa gtgcttagag 180

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<400> 27  
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 Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly Pro His  
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 His His His His Ile Glu Gly Arg Thr Pro Leu Gly Pro Ala Ser  
 35 40 45  
 Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
 50 55 60

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